

Application No.: 09/740,288  
Case No.: BB1429USNA(7560\*42)

Pag 2

**IN THE SPECIFICATION:**

Please replace the paragraph at page 4, lines 17-23 with the following rewritten paragraph:

D  
Figures 1A, 1B, and 1C shows a comparison of the amino acid sequences of the barley (SEQ ID NO:18), corn (SEQ ID NOs:20, 22, and 24), prickly poppy (SEQ ID NO:26), soybean (SEQ ID NOs:28 and 30), and wheat (SEQ ID NO:32) biotin synthase polypeptides to the enzymes from *Arabidopsis thaliana* (1705463, SEQ ID NO:33), fission yeast (*Schizosaccharomyces pombe*, 2995363, SEQ ID NO:34), and yeast (*Saccharomyces cerevisiae*, 6321725, SEQ ID NO:35). The conserved iron binding consensus sequence (GXCXEDCXYCXQ) is highlighted in italics and underlined (SEQ ID No:36).

Please replace the paragraph at page 25, lines 5-23 with the following rewritten paragraph:

B  
Figures 1A-1C shows a comparison of the amino acid sequences of the barley (SEQ ID NO:18), corn (SEQ ID NOs:20, 22, and 24), prickly poppy (SEQ ID NO 26), soybean (SEQ ID NOs:28 and 30), and wheat (SEQ ID NO:32) biotin synthase polypeptides to the enzymes from *Arabidopsis thaliana* (1705463, SEQ ID NO:33), fission yeast (*Schizosaccharomyces pombe*, 2995363, SEQ ID NO:34), and yeast (*Saccharomyces cerevisiae*, 6321725, SEQ ID NO:35). The conserved iron binding consensus sequence (GXCXEDCXYCXQ) is highlighted in italics and underlined black (SEQ ID No:36). The sequence for clone cdt2c.pk002.c17 (SEQ ID NQs:3, 4 and 19, 20) is very similar to the other two corn biotin synthase sequences with the exception of a 99 nucleotide deletion (33 amino acids) which includes the iron binding consensus motif (see Figures 1A-1C and 2). It is very likely that this cDNA clone represents a splice variant of the mRNA represented in SEQ ID NQ:21. The deleted sequence has consensus GT. . .AG intron border sequences, and the surrounding sequences fall within the requirements for a functional splice site junction. Whether this alternative splice product has any biological or regulatory role within the plant is unknown at this time. The second soybean sequence (SEQ ID NOs:13, 14 and 29, 30) is the only one analyzed in this group that shows higher homology to yeast biotin synthase genes than to plant biotin synthase sequences. The cDNA libraries that these clones were isolated from (sls1c, sls2c) were soybean tissues infected with the fungus *Sclerotinia*. It can not be ruled out that, this clone may represent a fungal rather than plant biotin synthase sequence.